

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/577, 658
Source: IFWP
Date Processed by STIC: 04/10/2007

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/10/2007

PATENT APPLICATION: US/10/577,658

TIME: 12:03:21

Input Set : A:\05081160.APP

Output Set: N:\CRF4\04102007\J577658.raw

4 <110> APPLICANT: CHABRIERE, ERIC
5 CONTRERAS-MARTEL, CARLOS
6 FONTECILLA-CAMPS, JUAN
8 <120> TITLE OF INVENTION: NEW PHOSPHATE-BINDING PROTEIN, PHARMACEUTICAL
9 COMPOSITIONS CONTAINING IT AND USES THEREOF
11 <130> FILE REFERENCE: 0508-1160
13 <140> CURRENT APPLICATION NUMBER: 10/577,658
14 <141> CURRENT FILING DATE: 2006-05-01
16 <150> PRIOR APPLICATION NUMBER: PCT/FR04/002797
17 <151> PRIOR FILING DATE: 2004-10-29
19 <150> PRIOR APPLICATION NUMBER: FR 03/12729
20 <151> PRIOR FILING DATE: 2004-10-30
22 <160> NUMBER OF SEQ ID NOS: 11
24 <170> SOFTWARE: PatentIn version 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 376
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: MOD_RES
33 <222> LOCATION: (1)..(1)
34 <223> OTHER INFORMATION: Asp or Ser
36 <220> FEATURE:
37 <221> NAME/KEY: MOD_RES
38 <222> LOCATION: (3)..(3)
39 <223> OTHER INFORMATION: Asn or Asp
41 <220> FEATURE:
42 <221> NAME/KEY: MOD_RES
43 <222> LOCATION: (11)..(11)
44 <223> OTHER INFORMATION: Gln or Glu
46 <220> FEATURE:
47 <221> NAME/KEY: MOD_RES
48 <222> LOCATION: (30)..(30)
49 <223> OTHER INFORMATION: Val or Thr
51 <220> FEATURE:
52 <221> NAME/KEY: MOD_RES
53 <222> LOCATION: (43)..(43)
54 <223> OTHER INFORMATION: Lys or Ser
56 <220> FEATURE:
57 <221> NAME/KEY: MOD_RES
58 <222> LOCATION: (50)..(50)
59 <223> OTHER INFORMATION: Asp or Asn
61 <220> FEATURE:

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Input Set : A:\05081160.APP

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62 <221> NAME/KEY: MOD_RES
63 <222> LOCATION: (54)..(54)
64 <223> OTHER INFORMATION: Asn or Asp
66 <220> FEATURE:
67 <221> NAME/KEY: MOD_RES
68 <222> LOCATION: (67)..(67)
69 <223> OTHER INFORMATION: Thr or Ser
71 <220> FEATURE:
72 <221> NAME/KEY: MOD_RES
73 <222> LOCATION: (68)..(68)
74 <223> OTHER INFORMATION: Glu or Gln
76 <220> FEATURE:
77 <221> NAME/KEY: MOD_RES
78 <222> LOCATION: (75)..(75)
79 <223> OTHER INFORMATION: Asp or Asn
81 <220> FEATURE:
82 <221> NAME/KEY: MOD_RES
83 <222> LOCATION: (77)..(77)
84 <223> OTHER INFORMATION: Glu or Gln
86 <220> FEATURE:
87 <221> NAME/KEY: MOD_RES
88 <222> LOCATION: (85)..(85)
89 <223> OTHER INFORMATION: Gln or Glu
91 <220> FEATURE:
92 <221> NAME/KEY: MOD_RES
93 <222> LOCATION: (102)..(102)
94 <223> OTHER INFORMATION: Ala or Gly
96 <220> FEATURE:
97 <221> NAME/KEY: MOD_RES
98 <222> LOCATION: (122)..(122)
99 <223> OTHER INFORMATION: Asp or Asn
101 <220> FEATURE:
102 <221> NAME/KEY: MOD_RES
103 <222> LOCATION: (143)..(143)
104 <223> OTHER INFORMATION: Ser or Val
106 <220> FEATURE:
107 <221> NAME/KEY: MOD_RES
108 <222> LOCATION: (219)..(219)
109 <223> OTHER INFORMATION: Thr or Ser
111 <220> FEATURE:
112 <221> NAME/KEY: MOD_RES
113 <222> LOCATION: (224)..(224)
114 <223> OTHER INFORMATION: Asp or Asn
116 <220> FEATURE:
117 <221> NAME/KEY: MOD_RES
118 <222> LOCATION: (252)..(252)
119 <223> OTHER INFORMATION: Val or Ser
121 <220> FEATURE:
122 <221> NAME/KEY: MOD_RES

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Input Set : A:\05081160.APP

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123 <222> LOCATION: (266)..(266)
 124 <223> OTHER INFORMATION: Asp or Asn
 126 <400> SEQUENCE: 1

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 128 1 5 10 15
 130 Pro Asp Val Leu Thr Ala Gly Phe Ala Pro Tyr Ile Gly Xaa Gly Ser
 131 20 25 30
 133 Gly Lys Gly Lys Ile Ala Phe Leu Glu Asn Xaa Tyr Asn Gln Phe Gly
 134 35 40 45
 136 Thr Xaa Thr Thr Lys Xaa Val His Trp Ala Gly Ser Asp Ser Lys Leu
 137 50 55 60
 139 Thr Ala Xaa Xaa Leu Ala Thr Tyr Ala Ala Xaa Lys Xaa Pro Gly Trp
 140 65 70 75 80
 142 Gly Lys Leu Ile Xaa Val Pro Ser Val Ala Thr Ser Val Ala Ile Pro
 143 85 90 95
 145 Phe Arg Lys Ala Gly Xaa Asn Ala Val Asp Leu Ser Val Lys Glu Leu
 146 100 105 110
 148 Cys Gly Val Phe Ser Gly Arg Ile Ala Xaa Trp Ser Gly Ile Thr Gly
 149 115 120 125
 151 Ala Gly Arg Ser Gly Pro Ile Gln Val Val Tyr Arg Ala Glu Xaa Ser
 152 130 135 140
 154 Gly Thr Thr Glu Leu Phe Thr Arg Phe Leu Asn Ala Lys Cys Thr Thr
 155 145 150 155 160
 157 Gln Pro Gly Thr Phe Ala Val Thr Thr Val Phe Ala Asn Ser Tyr Ser
 158 165 170 175
 160 Leu Gly Leu Ser Pro Leu Ala Gly Ala Val Ala Ala Ile Gly Ser Val
 161 180 185 190
 163 Gly Val Met Ala Ala Asp Asn Asp Val Thr Thr Ala Gln Gly Arg Ile
 164 195 200 205
 166 Thr Tyr Ile Ser Pro Asp Phe Ala Ala Pro Xaa Leu Ala Gly Leu Xaa
 167 210 215 220
 169 Asp Ala Thr Lys Val Ala Arg Thr Gly Lys Gly Ser Ser Ser Gly Gly
 170 225 230 235 240
 172 Gly Ala Glu Gly Lys Ser Pro Ala Ala Ala Asn Xaa Ser Ala Ala Ile
 173 245 250 255
 175 Ser Val Val Pro Leu Pro Ala Ala Ala Xaa Arg Gly Asp Pro Asn Val
 176 260 265 270
 178 Trp Thr Pro Val Phe Gly Ala Val Thr Gly Gly Gly Val Val Ala Tyr
 179 275 280 285
 181 Pro Asp Ser Gly Tyr Pro Ile Leu Gly Phe Thr Asp Leu Ile Phe Ser
 182 290 295 300
 184 Glu Cys Tyr Ala Asn Ala Thr Gln Thr Gly Gln Val Arg Asn Phe Phe
 185 305 310 315 320
 187 Thr Lys His Tyr Gly Thr Ser Ala Asn Asp Asn Ala Ala Ile Gln Ala
 188 325 330 335
 190 Asn Ala Phe Val Pro Leu Pro Ser Asn Trp Lys Ala Ala Val Arg Ala
 191 340 345 350
 193 Ser Tyr Leu Thr Ala Ser Asn Ala Leu Ser Ile Gly Asp Ser Ala Val
 194 355 360 365

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200 <210> SEQ ID NO: 2
201 <211> LENGTH: 376
202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 2
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207 1                      5                      10                      15
209 Pro Asp Val Leu Thr Ala Gly Phe Ala Pro Tyr Ile Gly Val Gly Ser
210      20                      25                      30
212 Gly Lys Gly Lys Ile Ala Phe Leu Glu Asn Lys Tyr Asn Gln Phe Gly
213      35                      40                      45
215 Thr Asp Thr Thr Lys Asn Val His Trp Ala Gly Ser Asp Ser Lys Leu
216      50                      55                      60
218 Thr Ala Thr Glu Leu Ala Thr Tyr Ala Ala Asp Lys Glu Pro Gly Trp
219 65                      70                      75                      80
221 Gly Lys Leu Ile Gln Val Pro Ser Val Ala Thr Ser Val Ala Ile Pro
222      85                      90                      95
224 Phe Arg Lys Ala Gly Ala Asn Ala Val Asp Leu Ser Val Lys Glu Leu
225      100                     105                     110
227 Cys Gly Val Phe Ser Gly Arg Ile Ala Asp Trp Ser Gly Ile Thr Gly
228      115                     120                     125
230 Ala Gly Arg Ser Gly Pro Ile Gln Val Val Tyr Arg Ala Glu Ser Ser
231      130                     135                     140
233 Gly Thr Thr Glu Leu Phe Thr Arg Phe Leu Asn Ala Lys Cys Thr Thr
234 145                     150                     155                     160
236 Gln Pro Gly Thr Phe Ala Val Thr Thr Val Phe Ala Asn Ser Tyr Ser
237      165                     170                     175
239 Leu Gly Leu Ser Pro Leu Ala Gly Ala Val Ala Ala Ile Gly Ser Val
240      180                     185                     190
242 Gly Val Met Ala Ala Asp Asn Asp Val Thr Thr Ala Gln Gly Arg Ile
243      195                     200                     205
245 Thr Tyr Ile Ser Pro Asp Phe Ala Ala Pro Thr Leu Ala Gly Leu Asp
246      210                     215                     220
248 Asp Ala Thr Lys Val Ala Arg Thr Gly Lys Gly Ser Ser Ser Gly Gly
249 225                     230                     235                     240
251 Gly Ala Glu Gly Lys Ser Pro Ala Ala Ala Asn Val Ser Ala Ala Ile
252      245                     250                     255
254 Ser Val Val Pro Leu Pro Ala Ala Ala Asp Arg Gly Asp Pro Asn Val
255      260                     265                     270
257 Trp Thr Pro Val Phe Gly Ala Val Thr Gly Gly Gly Val Val Ala Tyr
258      275                     280                     285
260 Pro Asp Ser Gly Tyr Pro Ile Leu Gly Phe Thr Asp Leu Ile Phe Ser
261      290                     295                     300
263 Glu Cys Tyr Ala Asn Ala Thr Gln Thr Gly Gln Val Arg Asn Phe Phe
264 305                     310                     315                     320
266 Thr Lys His Tyr Gly Thr Ser Ala Asn Asp Asn Ala Ala Ile Gln Ala
267      325                     330                     335

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269 Asn Ala Phe Val Pro Leu Pro Ser Asn Trp Lys Ala Ala Val Arg Ala
270          340          345          350
272 Ser Tyr Leu Thr Ala Ser Asn Ala Leu Ser Ile Gly Asp Ser Ala Val
273          355          360          365
275 Cys Gly Gly Lys Gly Arg Pro Glu
276          370          375
279 <210> SEQ ID NO: 3
280 <211> LENGTH: 376
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <400> SEQUENCE: 3
285 Ser Ile Asp Gly Gly Gly Ala Thr Leu Pro Glu Lys Leu Tyr Leu Thr
286 1          5          10          15
288 Pro Asp Val Leu Thr Ala Gly Phe Ala Pro Tyr Ile Gly Thr Gly Ser
289          20          25          30
291 Gly Lys Gly Lys Ile Ala Phe Leu Glu Asn Ser Tyr Asn Gln Phe Gly
292          35          40          45
294 Thr Asn Thr Thr Lys Asp Val His Trp Ala Gly Ser Asp Ser Lys Leu
295          50          55          60
297 Thr Ala Ser Gln Leu Ala Thr Tyr Ala Ala Asn Lys Gln Pro Gly Trp
298 65          70          75          80
300 Gly Lys Leu Ile Glu Val Pro Ser Val Ala Thr Ser Val Ala Ile Pro
301          85          90          95
303 Phe Arg Lys Ala Gly Gly Asn Ala Val Asp Leu Ser Val Lys Glu Leu
304          100          105          110
306 Cys Gly Val Phe Ser Gly Arg Ile Ala Asn Trp Ser Gly Ile Thr Gly
307          115          120          125
309 Ala Gly Arg Ser Gly Pro Ile Gln Val Val Tyr Arg Ala Glu Val Ser
310          130          135          140
312 Gly Thr Thr Glu Leu Phe Thr Arg Phe Leu Asn Ala Lys Cys Thr Thr
313 145          150          155          160
315 Gln Pro Gly Thr Phe Ala Val Thr Thr Val Phe Ala Asn Ser Tyr Ser
316          165          170          175
318 Leu Gly Leu Ser Pro Leu Ala Gly Ala Val Ala Ala Ile Gly Ser Val
319          180          185          190
321 Gly Val Met Ala Ala Asp Asn Asp Val Thr Thr Ala Gln Gly Arg Ile
322          195          200          205
324 Thr Tyr Ile Ser Pro Asp Phe Ala Ala Pro Ser Leu Ala Gly Leu Asn
325          210          215          220
327 Asp Ala Thr Lys Val Ala Arg Thr Gly Lys Gly Ser Ser Ser Gly Gly
328 225          230          235          240
330 Gly Ala Glu Gly Lys Ser Pro Ala Ala Ala Asn Ser Ser Ala Ala Ile
331          245          250          255
333 Ser Val Val Pro Leu Pro Ala Ala Ala Asn Arg Gly Asp Pro Asn Val
334          260          265          270
336 Trp Thr Pro Val Phe Gly Ala Val Thr Gly Gly Gly Val Val Ala Tyr
337          275          280          285
339 Pro Asp Ser Gly Tyr Pro Ile Leu Gly Phe Thr Asp Leu Ile Phe Ser
340          290          295          300

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/577,658

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1, 3, 11, 30, 43, 50, 54, 67, 68, 75, 77, 85, 102, 122, 143, 219, 224, 252

Seq#:1; Xaa Pos. 266

VERIFICATION SUMMARY

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L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

M:341 Repeated in SeqNo=1